

# Ming-Jing Hwang

## List of Publications by Year in descending order

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73  
papers

2,499  
citations

186265

28  
h-index

214800

47  
g-index

73  
all docs

73  
docs citations

73  
times ranked

3748  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of SUMO-Interacting Motif in Daxx SUMO Modification, Subnuclear Localization, and Repression of Sumoylated Transcription Factors. <i>Molecular Cell</i> , 2006, 24, 341-354.	9.7	374
2	Glucose-6-phosphate dehydrogenase (G6PD) mutations database: Review of the and update of the new mutations. <i>Blood Cells, Molecules, and Diseases</i> , 2012, 48, 154-165.	1.4	241
3	Derivation of Class II Force Fields. 4. van der Waals Parameters of Alkali Metal Cations and Halide Anions. <i>Journal of Physical Chemistry A</i> , 1997, 101, 7243-7252.	2.5	184
4	Detection and Classification of Cardiac Arrhythmias by a Challenge-Best Deep Learning Neural Network Model. <i>IScience</i> , 2020, 23, 100886.	4.1	106
5	Derivation of class II force fields. VIII. Derivation of a general quantum mechanical force field for organic compounds. <i>Journal of Computational Chemistry</i> , 2001, 22, 1782-1800.	3.3	84
6	Network position of hosts in food webs and their parasite diversity. <i>Oikos</i> , 2008, 117, 1847-1855.	2.7	75
7	Outer Membrane Protein I of <i>Pseudomonas aeruginosa</i> Is a Target of Cationic Antimicrobial Peptide/Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 8985-8994.	3.4	73
8	The role of microRNA in the delayed negative feedback regulation of gene expression. <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 722-726.	2.1	59
9	The N Terminus Domain of Type VI Adenylyl Cyclase Mediates Its Inhibition by Protein Kinase C. <i>Molecular Pharmacology</i> , 1999, 56, 644-650.	2.3	54
10	Mutations at KFRDI and V GK domains of enterovirus 71 3C protease affect its RNA binding and proteolytic activities. <i>Journal of Biomedical Science</i> , 2004, 11, 239-248.	7.0	53
11	The Role of Apoptosis Signal-regulating Kinase 1 in Lymphotoxin- $\beta$ Receptor-mediated Cell Death. <i>Journal of Biological Chemistry</i> , 2003, 278, 16073-16081.	3.4	52
12	Usefulness of Machine Learning-Based Detection and Classification of Cardiac Arrhythmias With 12-Lead Electrocardiograms. <i>Canadian Journal of Cardiology</i> , 2021, 37, 94-104.	1.7	45
13	Methods for Predicting Protein-Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2015, 1215, 383-398.	0.9	45
14	Oligomerization Is Crucial for the Stability and Function of Heme Oxygenase-1 in the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2009, 284, 22672-22679.	3.4	42
15	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	12.8	41
16	Primary Structure and Function Analysis of the <i>Abrus precatorius</i> Agglutinin A Chain by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2000, 275, 1897-1901.	3.4	39
17	Protein Kinase C Inhibits Type VI Adenylyl Cyclase by Phosphorylating the Regulatory N Domain and Two Catalytic C1 and C2 Domains. <i>Journal of Biological Chemistry</i> , 2002, 277, 15721-15728.	3.4	39
18	Lattice distortion by guest molecules in gas-hydrates. <i>Fluid Phase Equilibria</i> , 1993, 83, 437-444.	2.5	38

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19	Alternative alignments from comparison of protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 519-527.	2.6	38
20	A network perspective on the topological importance of enzymes and their phylogenetic conservation. <i>BMC Bioinformatics</i> , 2007, 8, 121.	2.6	38
21	Understanding system dynamics of an adaptive enzyme network from globally profiled kinetic parameters. <i>BMC Systems Biology</i> , 2014, 8, 4.	3.0	38
22	Luminal Galectin-9-Lamp2 interaction regulates lysosome and autophagy to prevent pathogenesis in the intestine and pancreas. <i>Nature Communications</i> , 2020, 11, 4286.	12.8	38
23	Territrein B, a Tremorogenic Mycotoxin That Inhibits Acetylcholinesterase with a Noncovalent yet Irreversible Binding Mechanism. <i>Journal of Biological Chemistry</i> , 1999, 274, 34916-34923.	3.4	36
24	An interaction-motif-based scoring function for protein-ligand docking. <i>BMC Bioinformatics</i> , 2010, 11, 298.	2.6	36
25	Topological and organizational properties of the products of house-keeping and tissue-specific genes in protein-protein interaction networks. <i>BMC Systems Biology</i> , 2009, 3, 32.	3.0	33
26	Plant Cytosolic Ascorbate Peroxidase with Dual Catalytic Activity Modulates Abiotic Stress Tolerances. <i>IScience</i> , 2019, 16, 31-49.	4.1	33
27	Site-directed mutagenesis evidence for a negatively charged trypsin inhibitory loop in sweet potato sporamin. <i>FEBS Letters</i> , 2001, 496, 134-138.	2.8	29
28	The dimeric transmembrane domain of prolyl dipeptidase DPP $\epsilon$ W contributes to its quaternary structure and enzymatic activities. <i>Protein Science</i> , 2010, 19, 1627-1638.	7.6	29
29	Ligand-binding site prediction using ligand-interacting and binding site-enriched protein triangles. <i>Bioinformatics</i> , 2012, 28, 1579-1585.	4.1	29
30	Novel indolizino[8,7-b]indole hybrids as anti-small cell lung cancer agents: Regioselective modulation of topoisomerase II inhibitory and DNA crosslinking activities. <i>European Journal of Medicinal Chemistry</i> , 2017, 127, 235-249.	5.5	23
31	BGN/TLR4/NF- $\kappa$ B Mediates Epigenetic Silencing of Immunosuppressive Siglec Ligands in Colon Cancer Cells. <i>Cells</i> , 2020, 9, 397.	4.1	23
32	Protomot: prediction of protein binding sites with automatically extracted geometrical templates. <i>Nucleic Acids Research</i> , 2006, 34, W303-W309.	14.5	22
33	Cleavage-site specificity of prolyl endopeptidase FAP investigated with a full-length protein substrate. <i>Journal of Biochemistry</i> , 2011, 149, 685-692.	1.7	22
34	GEM: A Gaussian evolutionary method for predicting protein side-chain conformations. <i>Protein Science</i> , 2002, 11, 1897-1907.	7.6	21
35	Protein structure comparison by probability-based matching of secondary structure elements. <i>Bioinformatics</i> , 2003, 19, 735-741.	4.1	21
36	LISE: a server using ligand-interacting and site-enriched protein triangles for prediction of ligand-binding sites. <i>Nucleic Acids Research</i> , 2013, 41, W292-W296.	14.5	21

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37	OPAAS: a web server for optimal, permuted, and other alternative alignments of protein structures. <i>Nucleic Acids Research</i> , 2006, 34, W95-W98.	14.5	20
38	Modeling Helix-Turn-Helix Protein-Induced DNA Bending with Knowledge-Based Distance Restraints. <i>Biophysical Journal</i> , 1999, 77, 1191-1205.	0.5	19
39	In silico identification and comparative analysis of differentially expressed genes in human and mouse tissues. <i>BMC Genomics</i> , 2006, 7, 86.	2.8	19
40	Epigenetic silencing of the synthesis of immunosuppressive Siglec ligand glycans by NF- $\kappa$ B/EZH2/YY1 axis in early-stage colon cancers. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 173-183.	1.9	15
41	PRAP1 is a novel lipid-binding protein that promotes lipid absorption by facilitating MTP-mediated lipid transport. <i>Journal of Biological Chemistry</i> , 2021, 296, 100052.	3.4	15
42	Tight Regulation of a Timed Nuclear Import Wave of EKLF by PKC $\delta$ and FOE during Pro-E to Baso-E Transition. <i>Developmental Cell</i> , 2014, 28, 409-422.	7.0	14
43	Single Nucleotide Polymorphism Mapping Using Genome-Wide Unique Sequences. <i>Genome Research</i> , 2002, 12, 1106-1111.	5.5	12
44	An Important Functional Role of the N Terminus Domain of Type VI Adenylyl Cyclase in G $\beta$ i-mediated Inhibition. <i>Journal of Biological Chemistry</i> , 2004, 279, 34440-34448.	3.4	12
45	Toward reducing immunogenicity of enzyme replacement therapy: altering the specificity of human $\beta$ -glucuronidase to compensate for $\beta$ -iduronidase deficiency. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 519-530.	2.1	12
46	An Analytical Rate Expression for the Kinetics of Gene Transcription Mediated by Dimeric Transcription Factors. <i>Journal of Biochemistry</i> , 2007, 142, 135-144.	1.7	11
47	Cbl-mediated K63-linked ubiquitination of JAK2 enhances JAK2 phosphorylation and signal transduction. <i>Scientific Reports</i> , 2017, 7, 4613.	3.3	11
48	Amino acid conservation and clinical severity of human glucose-6-phosphate dehydrogenase mutations. <i>Journal of Biomedical Science</i> , 1999, 6, 106-114.	7.0	10
49	On the use of distance constraints in protein-protein docking computations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 194-205.	2.6	10
50	Preservation of Ranking Order in the Expression of Human Housekeeping Genes. <i>PLoS ONE</i> , 2011, 6, e29314.	2.5	10
51	The UniMarker (UM) method for synteny mapping of large genomes. <i>Bioinformatics</i> , 2004, 20, 3156-3165.	4.1	9
52	Risk stratification for lung adenocarcinoma on EGFR and TP53 mutation status, chemotherapy, and PD-L1 immunotherapy. <i>Cancer Medicine</i> , 2019, 8, 5850-5861.	2.8	9
53	Conformational analysis of three pyrophosphate model species: Diphosphate, methyl diphosphate, and triphosphate. <i>Journal of Computational Chemistry</i> , 1999, 20, 1702-1715.	3.3	8
54	Directional shape complementarity at the protein-DNA interface. <i>Journal of Molecular Recognition</i> , 2003, 16, 213-222.	2.1	8

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55	Proteins with Highly Evolvable Domain Architectures Are Nonessential but Highly Retained. <i>Molecular Biology and Evolution</i> , 2016, 33, 1219-1230.	8.9	8
56	ALDH2 deficiency induces atrial fibrillation through dysregulated cardiac sodium channel and mitochondrial bioenergetics: A multi-omics analysis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166088.	3.8	8
57	Identification of Entry Factors Involved in Hepatitis C Virus Infection Based on Host-Mimicking Short Linear Motifs. <i>PLoS Computational Biology</i> , 2017, 13, e1005368.	3.2	8
58	New insights for dinucleotide backbone binding in conserved C5â€²-Hâ€²O hydrogen bonds. <i>Journal of Molecular Biology</i> , 1998, 279, 695-701.	4.2	7
59	A Critical Assessment of Information-guided Proteinâ€”Protein Docking Predictions. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 679-686.	3.8	7
60	A computational pipeline for identifying kinetic motifs to aid in the design and improvement of synthetic gene circuits. <i>BMC Bioinformatics</i> , 2013, 14, S5.	2.6	7
61	Artificial Intelligence-Enabled Electrocardiogram Improves the Diagnosis and Prediction of Mortality in Patients With Pulmonary Hypertension. <i>JACC Asia</i> , 2022, 2, 258-270.	1.5	7
62	Restraint-driven formation of $\beta$ -helical coiled coils in molecular dynamics simulations. , 1999, 50, 667-677.		6
63	The architectural design of networks of protein domain architectures. <i>Biology Letters</i> , 2013, 9, 20130268.	2.3	6
64	SLC38A2 Overexpression Induces a Cancerâ€”like Metabolic Profile and Cooperates with SLC1A5 in Panâ€”cancer Prognosis. <i>Chemistry - an Asian Journal</i> , 2020, 15, 3861-3872.	3.3	6
65	Novel Naturally Occurring Mutations of Enterovirus 71 Associated With Disease Severity. <i>Frontiers in Microbiology</i> , 2020, 11, 610568.	3.5	6
66	Usefulness of multi-labelling artificial intelligence in detecting rhythm disorders and acute ST-elevation myocardial infarction on 12-lead electrocardiogram. <i>European Heart Journal Digital Health</i> , 2021, 2, 299-310.	1.7	6
67	A model for Fis N-terminus and Fis-invertase recognition. <i>FEBS Letters</i> , 1997, 401, 1-5.	2.8	5
68	Proline in Transmembrane Domain of Type II Protein DPP-IV Governs Its Translocation Behavior through Endoplasmic Reticulum. <i>Biochemistry</i> , 2011, 50, 7909-7918.	2.5	3
69	Partitioning the Human Transcriptome Using HKera, a Novel Classifier of Housekeeping and Tissue-Specific Genes. <i>PLoS ONE</i> , 2013, 8, e83040.	2.5	3
70	NPPD: A Protein-Protein Docking Scoring Function Based on Dyadic Differences in Networks of Hydrophobic and Hydrophilic Amino Acid Residues. <i>Biology</i> , 2015, 4, 282-297.	2.8	3
71	Discovery of Recurrent Structural Motifs for Approximating Three-Dimensional Protein Structures. <i>Journal of the Chinese Chemical Society</i> , 2004, 51, 1107-1114.	1.4	2
72	JAK2-CHK2 signaling safeguards the integrity of the mitotic spindle assembly checkpoint and genome stability. <i>Cell Death and Disease</i> , 2022, 13, .	6.3	2

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73	A proteome view of structural, functional, and taxonomic characteristics of major protein domain clusters. Scientific Reports, 2017, 7, 14210.	3.3	1